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Genome size variation among recent human isolates of *Salmonella typhi*

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SUMMARY

We performed genome size estimation of 17 recent human isolates of *Salmonella typhi* from geographically diverse regions using pulsed-field gel electrophoresis (PFGE) after digestion of chromosomal DNA with restriction endonucleases *Xba*I (5'-TCTAGA-3'), *Avr*II (5'-CCTAGG-3') and *Spe*I (5'-ACTAGT-3'), and summation of the sizes of restriction fragments obtained. All 17 isolates had circular chromosomes, and genome sizes differed by as much as 959 kb, ranging from 3,964 to 4,923 kb (mean genome size = 4,528 kb). The data obtained confirm the usefulness of PFGE in studies of bacterial genome size and are in agreement with recent results indicating considerable genetic diversity and genomic plasticity of *S. typhi*. The variation in genome sizes noted may be relevant to the observed biological properties of this important human pathogen, including its virulence.

Key-words: Genome, *Salmonella typhi*; Virulence, Plasticity, Size variation, PFGE.

INTRODUCTION

Salmonella typhi, the cause of typhoid fever, remains a pathogen of major public health importance in many developing countries. Geographic variations in the clinical manifestations and severity of typhoid fever are well-documented, as is the varying efficacy of certain typhoid vaccine preparations in different endemic regions (Edelman and Levine, 1986). These observations of varying vaccine efficacy and differing disease severity have pointed to the possibility of the existence of strain variations among field isolates of *S. typhi* in endemic regions. We recently addressed this issue at the molecular level and demonstrated that considerable genetic diversity exists among recent human isolates of *S. typhi* in southeast Asia and other parts of the world (Thong *et al.*, 1994, 1995, 1996a). This was a significant development in light of a previous view that *S. typhi* represents a single clone that has shown minimal intraspecies divergence in its worldwide spread (Reeves *et al.*, 1989; Selander *et al.*, 1990). Interestingly, an association between molecular type and the ability to cause fatal and non-fatal typhoid fever has also been reported (Thong *et al.*, 1996b). Most importantly, the

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